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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/540,466

DATE: 04/15/2000
TIME: 09:48:39

Input Set: I540466.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

P.S.

ENTERED

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1  <110> APPLICANT: RIPAMONTI, UGO
2  RAMOSHEBI, LENTSHA N.
3  <120> TITLE OF INVENTION: METHODS FOR INDUCING ANGIOGENESIS USING MORPHOGENIC
4  PROTEINS AND STIMULATORY FACTORS
5  <130> FILE REFERENCE: STK-6
6  <140> CURRENT APPLICATION NUMBER: US/09/540,466
7  <141> CURRENT FILING DATE: 2000-03-31
8  <160> NUMBER OF SEQ ID NOS: 10
9  <170> SOFTWARE: PatentIn Ver. 2.1
10 <210> SEQ ID NO 1
11 <211> LENGTH: 1822
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
14 <220> FEATURE:
15 <221> NAME/KEY: CDS
16 <222> LOCATION: (49)..(1341)
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19                                     Met His Val
20                                     1
21   cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
22   Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
23       5                      10                      15
24   ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
25   Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
26       20                      25                      30                      35
27   gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
28   Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
29               40                      45                      50
30   cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
31   Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
32               55                      60                      65
33   ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
34   Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
35       70                      75                      80
36   ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc 345
37   Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
38       85                      90                      95
39   ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393
40   Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
41   100                      105                      110                      115
42   ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441
43   Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
44               120                      125                      130

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45	atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc	489
46	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
47	135 140 145	
48	cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc	537
49	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
50	150 155 160	
51	cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac	585
52	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
53	165 170 175	
54	tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat	633
55	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
56	180 185 190 195	
57	cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc	681
58	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
59	200 205 210	
60	gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac	729
61	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
62	215 220 225	
63	atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg	777
64	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
65	230 235 240	
66	ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc	825
67	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
68	245 250 255	
69	aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc	873
70	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
71	260 265 270 275	
72	ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc	921
73	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
74	280 285 290	
75	cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc	969
76	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
77	295 300 305	
78	aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc	1017
79	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
80	310 315 320	
81	agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc	1065
82	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
83	325 330 335	
84	cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc	1113
85	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
86	340 345 350 355	
87	gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg	1161
88	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
89	360 365 370	
90	aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac	1209
91	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
92	375 380 385	
93	ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc	1257
94	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	

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95          390          395          400
96  atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305
97  ile ser val leu tyr phe asp asp ser ser asn val ile leu lys lys
98          405          410          415
99  tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
100  tyr arg asn met val val arg ala cys gly cys his
101  420          425          430
102  gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411
103  gaaccagcag accaactgcc ttttgtgaga ctttcccctc cctatcccca actttaagg 1471
104  tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
105  atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac 1591
106  gcataaagaa aaatggccgg gccaggtcat tggtgaggaa gtctcagcca tgcacggact 1651
107  cgtttccaga ggtaattatg agcgctacc agccaggcca cccagccgtg ggaggaagg 1711
108  ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaaag gaaaattgac ccggaagttc 1771
109  ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaaa aaaaaaaaaa a 1822
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111  <211> LENGTH: 431
112  <212> TYPE: PRT
113  <213> ORGANISM: Homo sapiens
114  <400> SEQUENCE: 2
115  Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
116  1          5          10          15
117  Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
118  20          25          30
119  Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
120  35          40          45
121  Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
122  50          55          60
123  Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
124  65          70          75          80
125  Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
126  85          90          95
127  Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
128  100          105          110
129  Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
130  115          120          125
131  Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
132  130          135          140
133  Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
134  145          150          155          160
135  Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
136  165          170          175
137  Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
138  180          185          190
139  Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
140  195          200          205
141  Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Gly Trp Leu
142  210          215          220
143  Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
144  225          230          235          240

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145   His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
146               245               250               255
147   Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
148               260               265               270
149   Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
150               275               280               285
151   Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
152               290               295               300
153   Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
154   305               310               315               320
155   Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
156               325               330               335
157   Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
158               340               345               350
159   Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
160               355               360               365
161   Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
162               370               375               380
163   Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
164   385               390               395               400
165   Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
166               405               410               415
167   Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
168               420               425               430

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<210> SEQ ID NO 3

<211> LENGTH: 102

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: OPX

<220> FEATURE:

<223> OTHER INFORMATION: each Xaa is independently selected from a group of
 one or more specified amino acids as defined in
 the specification

<400> SEQUENCE: 3

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W--> 180   Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
181       1               5               10               15
W--> 182   Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
183               20               25               30
W--> 184   Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
185               35               40               45
W--> 186   Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
187               50               55               60
W--> 188   Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
189               65               70               75               80
W--> 190   Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
191               85               90               95
W--> 192   Xaa Ala Cys Gly Cys His
193               100

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<210> SEQ ID NO 4

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/540,466

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195 <211> LENGTH: 97
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-7
200 <220> FEATURE:
201 <223> OTHER INFORMATION: each Xaa is independently selected from a group of
202 one or more specified amino acids as defined in
203 the specification
204 <400> SEQUENCE: 4
W--> 205 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa
206 1 5 10 15
W--> 207 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
208 20 25 30
W--> 209 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa
210 35 40 45
W--> 211 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
212 50 55 60
W--> 213 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
214 65 70 75 80
W--> 215 Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
216 85 90 95
W--> 217 Xaa
218 <210> SEQ ID NO 5
219 <211> LENGTH: 102
220 <212> TYPE: PRT
221 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-8
224 <220> FEATURE:
225 <223> OTHER INFORMATION: each Xaa is independently selected from a group of
226 one or more specified amino acids as defined in the
227 specification
228 <400> SEQUENCE: 5
W--> 229 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
230 1 5 10 15
W--> 231 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
232 20 25 30
W--> 233 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
234 35 40 45
W--> 235 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
236 50 55 60
W--> 237 Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
238 65 70 75 80
W--> 239 Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
240 85 90 95
W--> 241 Xaa Xaa Cys Xaa Cys Xaa
242 100
243 <210> SEQ ID NO 6

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Please Note: <211> LENGTH: 97

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I540466.RAW

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180	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe X
182	W "N" or "Xaa" used: Feature required	Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa A
184	W "N" or "Xaa" used: Feature required	Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met A
186	W "N" or "Xaa" used: Feature required	Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa P
188	W "N" or "Xaa" used: Feature required	Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala X
190	W "N" or "Xaa" used: Feature required	Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys X
192	W "N" or "Xaa" used: Feature required	Xaa Ala Cys Gly Cys His
205	W "N" or "Xaa" used: Feature required	Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp X
207	W "N" or "Xaa" used: Feature required	Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa G
209	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His A
211	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
213	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa X
215	W "N" or "Xaa" used: Feature required	Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa V
217	W "N" or "Xaa" used: Feature required	Xaa
229	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe X
231	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa A
233	W "N" or "Xaa" used: Feature required	Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa X
235	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
237	W "N" or "Xaa" used: Feature required	Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa X
239	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa X
241	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Cys Xaa
254	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
256	W "N" or "Xaa" used: Feature required	Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa G
258	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
260	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
262	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa X
264	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
266	W "N" or "Xaa" used: Feature required	Xaa
278	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
280	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa X
282	W "N" or "Xaa" used: Feature required	Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
284	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
286	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa X
288	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
290	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Cys Xaa
303	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa
316	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa
327	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa Leu Xaa Val Xaa Phe X
329	W "N" or "Xaa" used: Feature required	Xaa Trp Xaa Xaa Xaa Pro Xaa Gly Xaa Xaa A
331	W "N" or "Xaa" used: Feature required	Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa X
333	W "N" or "Xaa" used: Feature required	Xaa Xaa Gln Xaa Xaa Val Xaa Xaa Xaa Asn X
335	W "N" or "Xaa" used: Feature required	Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa X
337	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa T
339	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Cys Xaa